KATIE SAUND
katiemsaund@gmail.com 313.418.3016 linkedin.com/in/katiesaund katiesaund.com github.com/katiesaund/

RESEARCH

Scientist in Discovery Genomics at Denali Therapeutics, South San Francisco, CA 2021 - Present
- computational biology, neurodegeneration (ALS, Alzheimer's Disease, Parkinson's Disease), multiomic biomarker discovery, machine learning, public datasets (Target ALS, AMP-PD, PPMI)

Intern with Genetics and Pharmacogenomics Department at Merck (Remote) Summer 2020
- single-cell RNA sequencing (scRNA-seq), early discovery oncology

PhD and Postdoctoral Fellow (Promoted 2020) at University of Michigan, Ann Arbor, MI 2015 – 2021
- bacterial genomics & metagenomics, infectious disease, R software development, microbiology, evolution

Research Assistant and Scientist I (Promoted 2014) at Seattle Children's Research Institute, Seattle, WA 2012 – 2015
- immunotherapy, solid tumor microenvironment, immuno-oncology, metabolism, NK cells & macrophages

Research Assistant at Project Peanut Butter, Blantyre, Malawi 2010 – 2011
- food & clinical interventions for pediatric malnutrition resolution

Research Fellow at Wayne State University, Detroit, MI 2009
- 16s rRNA alignment algorithm improvement, phylogenetic trees

EDUCATION

PhD in Microbiology & Immunology at University of Michigan, Ann Arbor, MI 2015 – 2020
- Awards: ASM Travel Award (2019), UM Rackham Conference Travel Grant (2019) & Professional Development Award (2019), NIH Predoctoral Genetics Training Grant (2016 – 2018), UM Maas Fellowship (2015).
- Roles: Wolverine Venture Fund, Undergraduate Honors Thesis Research Mentor

BS in Biology at California Institute of Technology, Pasadena, CA 2008 – 2012
- Awards: Everhart Service (2012), Teruggi Memorial (2011), Studenski Memorial (2010), & Shepard (2009).
- Leadership: Class of 2012 Co-President

PUBLICATIONS, PUBLICLY AVAILABLE SOFTWARE, & ORAL PRESENTATIONS

Select Publications:
- Saund, Pirani, Lacy, Hanna, Snitkin. mSphere. 2022.
- Saund & Snitkin. Microbial Genomics. 2020.
- Saund*, Lapp*, Thiede*, Pirani, Snitkin. Microbial Genomics. 2020. *Equal contribution.
- Saund, Rao, Young, Snitkin. Open Forum Infectious Diseases. 2020.

Software:
- prewas. R package. Data preprocessing for bacterial GWAS.
- hogwash. R package. Three bacterial GWAS methods.
- snitkitr. R package. Data analysis tools for bacterial genomics.

Oral Presentations:
- ASM Microbe (2019)
- NIAID Systems Biology and Antibacterial Resistance Program (2018)

COMPUTATIONAL AND LABORATORY SKILLS

Computational: R, bash, package development, cloud computing (AWS: EC2, S3, ECR. Google Cloud), Terra platform, Saturn Cloud, docker, conda, jupyter notebooks, high performance cluster (HPC) computing, batch scheduling (PBS, Slurm, Grid Engine), version control (git), data visualization, markdown, unit testing, linux/mac/PC, machine learning, transcriptomics (bulk, single-cell, single-nuclei, splicing, deconvolution), genomics, metabolomics, surrogate variable analysis, multiomic integration

Laboratory: CRISPR/Cas9 genome editing, cryostat, ELISA, experimental design, flow cytometry, immune cell isolation (cell sorting, magnetic enrichment), lentiviral transduction, mammalian cell culture, molecular biology (Gibson assembly, transfection, Western blot, qPCR), mouse handling: experimental autoimmune encephalomyelitis (multiple sclerosis mouse model), microbial techniques (anaerobic bacterial culture, bacterial stains), plasmid construction, protein co-immunoprecipitation, robotic pipetting system